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O.G. FIG.

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GCGCACTATGAAGGCCACAAGATCATTGAGATTGGTGCCGTTGAAGTGGTGAACCGTCGCCTGACGGGCAATAAC 150 225 300 375 75 ATGACCGCTATGAGCACTGCAATTACACGCCAGATCGTTCTCGATACCGAAACCACCGGTATGAACCAGATTGGT TCCATGITTATCTCAAACCCGATCGGCTGGTGGATCCGGAAGCCTTTGGCGTACATGGTATTGCCGATGAATTT TGCTCGATAAGCCCACGTTTGCCGAAGTAGCCGATGAGTTCATGGACTATATTCGCGGCGCGGGAGTTGGTG CATAACGCAGCGTTCGATATCGGCTTTATGGACTACGAGTTTTCGTTGCTTAAGCGCGATATTCCGAAGACCAAT G Z Z Z Σ 4 ය œ ය ර α œ Z mutD Σ ഗ -mutD -mutD mutD--mutD Ø ш ග 0 œ ш α u × G ⋖ ۵. I ഗ ග ۵. Σ ⋖ エ I Σ

FIG._ 1A

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SUBCLASS <u>ACTTTCTGTAAGGTCACCGATAGCCTTGCGGTGGCGAGGAAATGTTTCCCGGTAAGCGCAACAGCCTCGATGCG</u> 450 TTATGTGCTCGCTACGAAATAGATAACAGTAAACGAACGCTGCACGGGGCATTACTCGATGCCCAGATCCTTGCG 525 GAAGTITATCTGGCGATGACCGGTGGTCGATGGCTTTTGCGATGGAGGAGGAGACACACAACAGCAACAA 600 GGTGAAGCAACAATTCAGCGCATTGTACGTCAGGCAAGTTACGCGTTGTTTTTGCGACAGATGAAGAGATT 675 APPROVED O.G. FIG. CLASS O DRAFTSMAN w GCAGCTCATGAAGCCCGTCTCGATCTGGTGCAGAAGAAGGCGGAAGTTGCCTCTGGCGAGCATAA 741 ձ 0 ഗ O O Z ⋖ œ The state of the s Ø ය G W 4 Σ ග Ø œ ഗ エ щ G G mutD -mutD -mutD œ mutD Σ ဟ ⋖ œ ഗ ⋖ -mutD. ¥ O ഗ 0 œ Z 9 ഗ œ ш Σ œ > ⋖ Þ \mathbf{x} œ Ø エ نيا

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FIG._ 1B

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09 60 60 60 60 60 60 60 60 60 60 60 60 60	120	GCCTGCTGGTGACC	G T G A A G C A C C T G A A A G T G A C C C T G A A A	240	C C G A A A G A C A C C A A C C C G A A A G A C A C	300 ATAATCACCGTCGGC ATAATCACCGTCGGC
50 G T G A A C T T C	110 G T A A A A A A A A A A A A A A A A A A	G T A A A A A A A 170	A T C A G A C C	230 -	A G C C G A A C A G C C G A A C	290 G C G A C A T G G C G A C A T G
GGTTCCAAAT	100 1 G C T G G	A G C T G C T G G G G C C	0 6 6 7 6 C 7 6 7 C 6 C 6 C 7 6 7 C 6 C 7 6 7 C 7 C	220 1	C G A C G G G G T C G C G A C G G G G T C G	ZBO TAAAGAGCAGT TAAAGAGCAGT
30 TTGATTATCT TTGATTATCT	90	A G C G C T G C C	CCATTAAAGA CCATTAAAGA	210	TGGTCATTTT TGGTCATTTT	CCATGTTCGT CCATGTTCGT
20 CTATCGTATGT CTATCGTATGT	80	G T T G T T G G C 140	6 6 C C T 6 C 6 C 6	200	G G T A T T G A G G G G T A T T G A G G	260 G A C G G C C T G G
10 10 ATGAGO 10 ATGAGO	70 GITICI	6 1 1 1 C	130 GATAAG	190	190 6 C G C C C C C C C C C C C C C C C C C	250 G T G C T C 250 G T G C T C

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310 310	0 0 C 0 0 C A 0 C C O C A C C C O C C A C C C O C A C C C C A C C C C C C A C	CCGCACGA	C T G C G G T A A A G C T G C G G T A A A G	GCATTGGTATT	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	A C C C G G G T G A T A C C C G G G T G A T	Eb_429T.dna Eb_GEBT.dna	
	370	380	390	400	410	420	i	
370 370	CTGTACAG	CTATGCCGG CTATGCCGG	TATCGAAACAC TATCGAAACAC	T C A C C A A C C	CGCTGCCGCCCA	TTATTGCGGTC TTATTGCGGTC	- Eb_429T.dna Eb_GEBT.dna	·
	430	440	450	460	470	480		
430 430	AACACCAC)	C G C C A G C G A A G	T C A C C C C C C A C	16 C G T G C T G A	CTAACACCAAA	Eb_429T.dna Eb_GEBT.dna	4/10
	490	500	510	520	530	540		
490 490	ACCAAAG	TAAAATTTGTG TAAAATTTGTG	ATTGTCAGCT ATTGTCAGCT	G G C G C A A C C T G G G C G C A A C C T G	CCTTCCGTCT	CCATTAACGAT	Eb_429T.dna Eb_GEBT.dna	
	550	560	570	580	590	009		
550 550	6	T G A T G A T C G C C I G A T G A T C G C C I	A A G C C C G C C G	GGCTGACCGCCGC	GCCACCGGTA	TGGATGCCTG	Eb_429T.dna Eb_GEBT.dna	

FIG._2B

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CCAAAGACGCCAACCGGTTACCGATGCCTCTGCT Eb_429T.dna CCAAAGACGCCAACCGGTTACCGATGCCTCTGCT Eb_6EBT.dna 700 710 720 CCAACTTGCGCCAGGCCGTCGCCCTGGGGACCAAC Eb_429T.dna CCAACTTGCGCCAGGCCGTCGCCTGGGGACCAAC Eb_429T.dna 760 770 780 GCGCCTCTCTGTGCCGGATGGCCTTTAACAAC Eb_429T.dna GCGCCTCTCTGTGGCGGATGGCCTTTAACAAC Eb_429T.dna GCGCTCTCTGTGGCGGGTTAACGAC Eb_429T.dna IGGCTCACCAGCTGGCGGGTTAACGACATGGCC Eb_6EBT.dna IGGCTCACCAGCTGGCGGCTGTACGACATGGCC Eb_6EBT.dna IGGCTCACCAGCTGGCGCTGTACGACATGGCC Eb_6EBT.dna IGGCTCACCAGCTGGCCTGTACGACATGGCC Eb_6EBT.dna 880 890 900
700 710 720 A A C T T G C G C C A G G C C G T C G C C T G G G A (A A C T T G C C C A G G C C G T C G C C T G G G A (760 770 780 G C C T C T C T G C T G G C C G G G A T G G C C T T T A A G C T C T C T G C G G G T G G C C T T T A A G C T C A C G C G G C C T G T A C G A C A T G C T C A C C A C C T C A C C A C C T C A C C A C C C G G C C C T G T A C G A C A T G C T C A C C A C C C C G G C C C T G T A C G A C A T G C T C A C C A C C C C C G C C C T G T A C G A C A T G C T C A C C C C C C C C C C C C C C C C
CCACCAACTTGCGCCAGGCCGTCGCCCTGGGGACCAA CCACCAACTTGCGCCAGGCCGTCGCCCTGGGGACCAA 760 770 780 CCTGCGCTCTCTGCTGGCCGGATGGCCTTTAACAA CCTGCGCTCTTTAACAA CCTGCGCTCTTTAACAA CCTGCGCTCTTTAACAA CCTGCGCTCTTTAACAA CCTGCGCTCTTTAACAA CCATGGCTCACCAGCTGGGCGGCTGTACGACATGGCCCATGGCTCATGGCCCATGGCCTTTACGACATGGCCCATGGCTCATGGCCCATGGCCTGTACGACATGGCCCATGGCCCATGGCCTGTACGACATGGCCCATGGCTCATGGCCTCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCTCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCTGTACGACATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCTGTACGCCTGTACGCCTCATGGCCCATGGCCCATGGCCTCATGGCCTGTACGCCTGTACGCCTATGGCCCATGGCCCATGGCCTGTACGCCTGTACGCCTGTACGCCCATGGCCCATGGCCCTGTACGCCTGTACGCCTGTACGCCTGTACGCCCATGGCCCATGGCCCTGTACGCCTGTACGCCTGTACGCCTGTACGCCCATGGCCCATGGCCCATGGCCTGTACGCCTGTACGCCTGTACGCCCATGGCCCATGGCCTGTACGCCTGTACGCCTGTACGCCCATGGCCCATGGCCCATGGCCTGTACGCCTGTACGCCTGTACGCCCATGGCCCATGGCCCATGGCCCATGGCCTGTACTGCCCATGGCCCATGGCCCATGGCCTGTACTGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGCTACTGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGCCATGGCCCATGCCCATGCCCATGCCATGCCCATGCCCATGCCATGCCATGCCATGCCCATGCCCATGCCCATGCCCATGCCCATGCCCATGCCCATGCCATGCCATGCCATGCCATGCCCATGCCATGCCATGCCCATGCATG
760 770 780 CCTGCGCTCTCTGCTGGCGGGATGGCCTTTAACA CCTGCCTCTCTGTGGCCGGATGGCTTTAACA 820 830 840 CCATGGCTCACCAGCTGGGCGCCTGTACGACATGG CCATGGCTCACCAGCTGGGCGCCTGTACGACATGG CCATGGCTCACCAGCTGGGCGCCTGTACGACATGG CCATGGCTCACCAGCTGGGCGCCTGTACGACATGG 880 890 900
CCTGCGCTCTCTGCTGGCCGGGATGGCCTTTAACA CCTGCGCTCTTTAACA 820 830 840 CCATGGCTCACCAGCTGGCGTTTAGG CCATGGCTCACCAGCTGGCGCCTGTACGGCCCTTTGG
CCATGGCTCACCAGCTGGGCGGCCTGTACGACAT CCATGGCTCACCAGCTGGGCGGCCTGTACGACAT CCATGGCTCAGCTGGGCGCCTGTACGACAT
CCATGGCTCACCAGCTGGGCGGCCTGTACGACATGGCC CCATGGCTCACCAGCTGGGCGGCCTGTACGACATGGCC
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FIG._2C

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	7	920	930	940),	950	096	
910	C C G G A A A A A A A A A A A A A A A A	ATTTGCCGATA ATTTGCCGATA	A T C G C C A C C T T A T C G C C A C C T T	TATGGGGGAAA TATGGGGGAAA	ACACCACGGT	1 1 1 1 1 1 1	CCACC Eb_429T.dna
	970	086	066	1000	1010	1020	
970 970	A T G G A C G C A A T G G A C G C A	GCGGAGCTGG	CCATCAGCGC	CATTGCCCGTC	T G T C T A A A G T G T C T A A A G	A T G T C G G G A T C A T G T C G G G A T C	Eb_429T.dna Eb_GEBT.dna
	1030	1040	1050	1060	1070	1	5 5
1030	C C G C A G C A C	CTGCGTGAAC CTGCGTGAAC	T G G G G G T A A A T G G G G G G T A A A	A G A G G C G A C T A G A G G C C G A C T	T C C C G T A C A T T C C C G T A C A T	GGCAGAAATG	Eb_429T.dna S
	1090	1100	1110	1120 1	1130	1140	
1090	GCCCTGAAAGCCCTGAAA	G A C G G C A A C G G A C G G C A A C G	CCTTCTCTAA	CCCGCGCAAAG	GGGAACGAAAA	A G A T T G C C A G A T T G C C	Eb_429T.dna Eb_GFBT.dna
	1150	1160	1170)	
1150 1150	GACATTTTC GACATTTTC	CGCCAGGCAT	TCTGA				Eb_429T.dna
2000		: :				_	ED_GEBI.dna

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIG._2D

-	Eb_GEBT.dna	Eb_429T.dna Eb_GEBT.dna	Eb_429T.dna Eb_GEBT.dna	Eb_429T.dna Eb_GEBT.dna	Eb_429T.dna Eb_GEBT.dna
	SYRMFDYLVPNVNFFGPGAVSVVGQRCQLLGG	/ DQTVKHLKAAGIEVVIFDGVEPNPKDTN/ DQTVKHLKAAGIEVVIFDGVEPNPKDTN	JAO DGLAMFRKEQCDMIITVGGGSPHDCGKGIGIAATHPGD DGLAMFRKEQCDMIITVGGGSPLDCGKGIGIAATHPGD	1370 460 430 460 LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLTNTK LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLTNTK	TKVKFVIVSWRNLPSVSINDPLLMIGKPAGLTAATGMDAL
0	0	130	250	370 370	490

FIG._3A

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		- Eb_429T.dna Eb_GEBT.dna		Eb_429T.dna Eb_GEBT.dna		Eb_429T.dna Eb_GEBT.dna		Eb_429T.dna Eb_GEBT.dna		Eb_429T.dna Eb_GEBT.dna
	200	A T N L R Q A V A L G T N A T N L R Q A V A L G T N	820	A M A H Q L G G L Y D M A A M A H Q L G G L Y D M A	940	TEMGENTIGLST	1060	V K B A D P P Y M A B M V K B A D P P Y M A B M		
	67,0	T D A S A I Q A I K L I I	790	M A F N N A N L G Y V H P M A F N N A N L G Y V H P	910	N L I A N P E K F A D I A N L I A N P E K F A D I A	1030	DVGIPQHLRELG DVGIPQHLRELG	1150	K E I A D I P R Q A F. K E I A D I P R Q A F.
	640	AYISKDANPV AYISKDANPV	760	N M A C A S L L A G P N M A C A S L L A G P	880 -	A V L L P H V C R Y N A V L L P H V C R Y N	1000	LAISAIARLSK LAISAIARLSK	1120	IAFSNPRKGNE IAFSNPRKGNE
-8	010	610 THAVE 610 THAVE	730	730 LKARE 730 LKARE	850 -	850 H G V A N 850 H G V A N	970	970 MDAAE1 970 MDAAE1	1090	1090 ALKDGN 1090 ALKDGN

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

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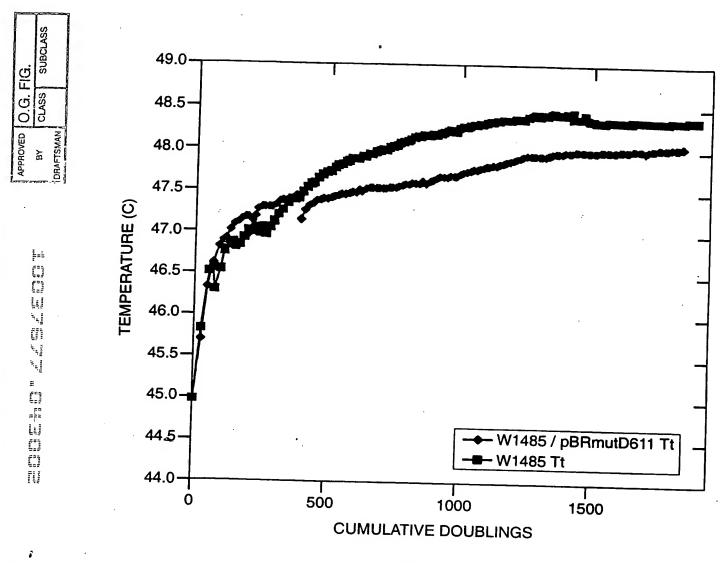


FIG._4

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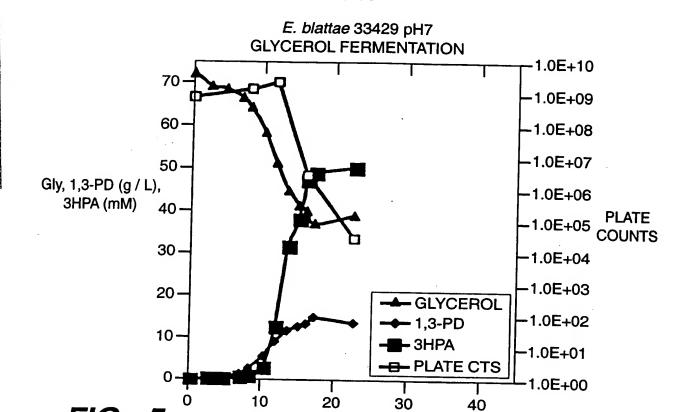
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